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SEQUENCE LISTING

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	a agt tat n Ser Tyr 35	-									-	144
	t ctt gaa o Leu Glu		_	_	_		=					192
	t aca cca s Thr Pro		_			_			_			240
	t tat cag l Tyr Gln			_								288
	t tta tat n Leu Tyr 100	=	_									336
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	c atg aca r Met Thr 0		_				_				_	432
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tca tat ctg gcg Ser Tyr Leu Ala		ı Phe Ser (-	528
gca tca aga gca Ala Ser Arg Ala 180		_	_			576
cgg ttc agg caa Arg Phe Arg Gln 195						624
gct cct gtt tat Ala Pro Val Tyr 210		r Pro Glu A	= =	Leu Thr	-	672
tgg ggg aga atc Trp Gly Arg Ile 225	_		= = =		_	720
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act gtg gcc gtt Thr Val Ala Val 260				_	_	816
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Gln	Gln	Ser 35	Tyr	Val	Ser	Ser	Leu 40	Asn	Ser	Ile	Arg	Thr 45	Val	Ile	Ser
Thr	Pro 50	Leu	Glu	His	Ile	Ser 55	Gln	Gly	Ala	Thr	Ser 60	Val	Ser	Val	Ile
Asn 65	His	Thr	Pro	Pro	Gly 70	Ser	Tyr	Ile	Ser	Val 75	Gly	Ile	Arg	Gly	Leu 80
Asp	Val	Tyr	Gln	Glu 85	Arg	Phe	Asp	His	Leu 90	Arg	Leu	Ile	Ile	Glu 95	Arg
Asn	Asn	Leu	Tyr 100	Val	Ala	Gly	Phe	Val 105	Asn	Thr	Thr	Thr	Asn 110	Thr	Phe
Tyr	Arg	Phe 115	Ser	Asp	Phe	Ala	His 120	Ile	Ser	Leu	Pro	Gly 125	Val	Thr	Thr
Ile	Ser 130	Met	Thr	Thr	Asp	Ser 135	Ser	Tyr	Thr	Thr	Leu 140	Gln	Arg	Val	Ala
Ala 145	Leu	Glu	Arg	Ser	Gly 150	Met	Gln	Ile	Ser	Arg 155	His	Ser	Leu	Val	Ser 160
Ser	Tyr	Leu	Ala	Leu 165	Met	Glu	Phe	Ser	Gly 170	Asn	Thr	Met	Thr	Arg 175	Asp
Ala	Ser	Arg	Ala 180	Val	Leu	Arg	Phe	Val 185	Thr	Val	Thr	Ala	Glu 190	Ala	Leu
Arg	Phe	Arg 195	Gln	Ile	Gln	Arg	Glu 200	Phe	Arg	Leu	Ala	Leu 205	Ser	Glu	Thr
Ala	Pro 210	Val	Tyr	Thr	Met	Thr 215	Pro	Glu	Asp	Val	Asp 220	Leu	Thr	Leu	Asn
Trp 225	Gly	Arg	Ile	Ser	Asn 230	Val	Leu	Pro	G1u	Tyr 235	Arg	Gly	Glu	Ala	Gly 240
Val	Arg	Val	Gly	Arg 245	Ile	Ser	Phe	Asn	Asn 250	Ile	Ser	Ala	Ile	Leu 255	Gly

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Thr Val Ala Val Ile Leu Asn Cys Gly Asn Ser Ser Arg Thr Ile Thr 260 265 270 Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu 280 285 275 Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln 290 295 300 Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu 315 305 310 <210> 3 <211> 1325 <212> DNA <213> Escherichia coli <220> <221> CDS <222> (951)..(1322) <400> 3 60 atgatgaagt gtatattgtt aaagtggata ctgtgtctgt tactgggttt ttcttcggta 120 tectattece aggagtttae gatagaettt tegaeteaae aaagttatgt atettegtta 180 aatagtatac ggacagtgat atcgacccct cttgaacata tatctcaggg agctacatcg 240 gtatccgtta ttaatcatac accaccagga agttatattt ccgtaggtat acgagggctt gatgtttatc aggagcgttt tgaccatctt cgtctgatta ttgaacgaaa taatttatat 300 360 gtggctggat ttgttaatac gacaacaaat actttctaca gattttcaga ttttgcacat 420 atatcattgc ccggtgtgac aactatttcc atgacaacgg acagcagtta taccactctg 480 caacgtgtcg cagcgctgga acgttccgga atgcaaatca gtcgtcactc actggtttca 540 tcatatctgg cgttaatgga gttcagtggt aatacaatga ccagagatgc atcaagagca 600 gttctgcgtt ttgtcactgt cacagcagaa gccttacggt tcaggcaaat acagagagaa tttcgtctgg cactgtctga aactgctcct gtttatacga tgacgccgga agacgtggac 660 720 ctcactctga actgggggag aatcagcaat gtgcttccgg agtatcgggg agaggctggt 780 gtcagagtgg ggagaatatc ctttaataat atatcagcga tacttggtac tgtggccgtt 840 atactgaatt gtggaaattc atcaagaaca atcacaggtg atacttgtaa tgaggagacc 900 cagaatctga gcacaatata tctcagggaa tatcaatcaa aagttaagag gcagatattt 956 tcagactatc agtcagaggt tgacatatat aacagaattc gggatgaatt atg aat Met Asn 1 aaa gta aaa tgt tat gtt tta ttt acg gcg tta cta tcc tct cta tat 1004 Lys Val Lys Cys Tyr Val Leu Phe Thr Ala Leu Leu Ser Ser Leu Tyr

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-			tt aca ttt aag agc ggc 1148 le Thr Phe Lys Ser Gly 65
-	- -		aa cat ata gac tcc cag 1196 ln His Ile Asp Ser Gln 80
			ta aga atc aca tat ctg 1244 eu Arg Ile Thr Tyr Leu 95
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100 105 110

Thr Pro Asn Ser Ile Ala Ala Ile Ser Met Lys Asn 115 120